

GCTCTCCCTGCTCCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTG  
M R A L E G P G L S L L

TGCCTGGTGTGGCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAA  
C L V L A L P A L L P V P A V R G V A E

ACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGC  
 T P T Y P W R D A E T G E R L V C A Q C

CCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCCG  
 P P G T F V Q R P C R R D S P T T C G P

TGTCCACCGCGCCACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAAC  
 C P P R H Y T Q F W N Y L E R C R Y C N

GTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCC  
 V L C G E R E E E A R A C H A T H N R A

TGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGT  
 C R C R T G F F A H A G F C L E H A S C

CCACCTGGTGCCGGCGTGATTGCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCG  
 P P G A G V I A P G T P S Q N T Q C Q P

TGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGC  
 C P P G T F S A S S S S S E Q C Q P H R

AACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTG  
 N C T A L G L A L N V P G S S S H D T L

TGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG  
 C T S C T G F P L S T R V P G A E E C E

CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTG  
 R A V I D F V A F Q D I S I K R L Q R L

CTGCAGGCCCTCGAGGCCCGGAGGGCTGGGCTCCGACACCAAGGGCGGGCCGCGCGGCC  
 L Q A L E A P E G W G P T P R A G R A A

TTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTG  
 L Q L K L R R R L T E L L G A Q D G A L

CTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTC  
 L V R L L Q A L R V A R M P G L E R S V

CGTGAGCGCTTCTCCCTGTGCACTGATCCTGGCCCCCTTATTTATTCTACATCCTTG  
 R E R F L P V H \*

GCACCCCACTTGCACTGAAAGAGGCTTTTTTTTAAATAGAAGAAATGAGGTTTCTTAAAG

CTTATTTTTATAAAGCTTTTTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG.1

2/23

TGGCATGTCGGTCAGGCACAGCAGGGTCCTGTGTCCGCGCTGAGCCGCGCTCTCCCTGCT  
CCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTGCTGCTGTGCCTGGTGTG  
M R A L E G P G L S L L C L V L  
GCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTAC  
A L P A L L P V P A V R G V A E T P T Y  
CCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACC  
P W R D A E T G E R L V C A Q C P P G T  
TTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGC  
F V Q R P C R R D S P T T C G P C P P R  
CACTACACGCAGTTCTGGAACCTGAGCGCTGCCGCTACTGCAACGTCTCTGCGGG  
H Y T Q F W N Y L E R C R Y C N V L C G  
GAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCTGCCGCTGCCGC  
E R E E E A R A C H A T H N R A C R C R  
ACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCC  
T G F F A H A G F C L E H A S C P P G A  
GGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGGGCCCCAGGAGTGGTGGCCGG  
G V I A P G E S W A R G G A P R S G G R  
AGGTGTGGCAGGGGTCAGGTTGCTGGTCCCAGCCTTGACCCTGAGCTAGGACACCAAGTT  
R C G R G Q V A G P S L A P \*  
CCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCAGAACACGCAGTGCCA  
GCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCA  
CCGCAACTGCACGGCCCTGGGCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACAC  
CCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCAGAGGC  
CTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCTGCACG  
TGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTGAGGGG  
TCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAGAATTT  
GGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCAATCTCC

FIG.2A

0993727-092404  
T04280-225660

TAACTGCCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTGATGGT  
AACTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAAACCGAGGC  
CCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTGACCCCTTAACATCAAGTCAG  
GTCCGGTCCATCTGCAGGTCCCAACTCGCCCCCTTCGATGGCCCAGGAGCCCCAAGCCCT  
TGCCTGGGCCCCCTTGCCCTTTGCAGCCAAGGTCCGAGTGGCCGCTCCTGCCCCCTAGGC  
CTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCCTTCTCCAGTCCCCATCGTTGCACT  
GCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCCGAGTGG  
GGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGTGGGTGAAATGATCGGAC  
CGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTATCGACTTTG  
TGGCTTTCCAGGACATCTCCATCAAGAGGAGCGGCTGCTGCAGGCCC

FIG.2B

1	M	G	L	S	T	V	P	D	L	L	L	P	L	V	L	E	L	L	V	G	I	Y	P	S	G	V	I	G	L	V	P	H	L	G	D	R	E	-	TNFR1		
1	M	A	P	V	A	T	W	A	A	L	A	V	G	L	E	L	W	A	A	H	A	L	P	A	Q	V	A	-	-	-	-	-	-	F	T	P	-	-	TNFR2		
1	M	G	A	G	A	T	R	A	M	D	-	-	-	G	P	R	L	L	L	L	L	L	L	G	V	S	L	G	A	K	E	-	A	C	P	-	-	NGFR			
1	M	-	R	L	P	R	-	A	S	S	P	C	G	L	A	W	G	P	L	L	L	L	S	G	L	L	V	A	S	Q	P	Q	L	V	P	P	-	-	LTbR		
1	M	L	G	I	W	-	-	-	-	L	L	P	-	-	L	V	L	T	S	V	-	A	R	L	S	S	K	S	V	N	A	Q	V	T	D	I	N	S	K	L	FAS
1	M	-	-	-	-	A	R	P	H	P	-	-	-	-	W	W	L	C	V	L	G	T	L	V	G	L	S	-	A	T	P	A	P	K	S	C	P	-	-	CD27	
1	M	R	V	R	L	-	-	-	-	-	-	-	-	-	L	A	A	L	G	L	L	F	L	G	A	L	R	-	-	-	-	-	-	F	P	Q	-	-	CD30		
1	M	V	R	L	P	L	-	-	-	-	-	-	-	-	L	-	W	G	C	L	L	-	-	-	-	T	A	V	H	P	E	-	-	P	P	-	-	CD40			
1	M	G	N	-	-	-	-	-	-	-	-	-	-	-	L	-	V	A	T	L	L	L	V	L	N	-	-	-	-	-	-	-	-	F	E	R	-	-	4-1BB		
1	M	C	V	G	A	-	-	-	-	-	-	-	-	-	R	G	P	C	A	A	L	L	L	G	L	G	L	S	T	V	T	G	L	H	C	V	-	-	OX40		
1	M	K	S	V	-	L	Y	L	I	-	-	-	-	-	L	F	S	C	I	I	I	N	G	R	D	A	A	P	-	-	-	-	-	Y	T	P	-	-	VC22		
1	M	K	S	-	-	-	Y	I	L	L	-	-	-	-	L	L	L	S	C	I	I	I	N	S	D	I	T	P	-	-	-	-	-	H	E	P	-	-	CRMB		
1	M	R	A	L	E	-	-	-	-	-	-	-	-	-	L	L	C	L	V	L	A	L	P	A	L	L	P	-	-	-	-	-	-	V	P	A	-	-	TNFR-6a		
1	M	R	A	L	E	-	-	-	-	-	-	-	-	-	L	L	C	L	V	L	A	L	P	A	L	L	P	-	-	-	-	-	-	V	P	A	-	-	TNFR-6b		

FIG.3A

39	-	K	R	D	S	V	C	P	Q	G	K	Y	I	H	-	-	P	Q	N	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	Y	N	D	C	P	G	TNFR1		
32	-	Y	-	A	P	E	P	G	S	T	C	R	L	R	E	Y	-	D	Q	T	A	Q	M	C	C	S	K	C	S	P	G	Q	H	A	K	V	F	C	-	TNFR2		
34	-	T	-	-	-	-	-	-	-	-	-	-	-	-	G	L	Y	T	H	S	G	E	-	C	C	K	A	C	N	L	G	E	G	V	A	Q	P	C	G	ANGFR		
36	-	Y	R	I	E	N	Q	T	C	W	D	Q	D	K	E	Y	E	P	M	H	D	V	F	C	C	S	R	C	P	P	P	G	E	F	V	F	A	V	C	-	LbR	
36	E	L	R	K	T	V	-	-	-	-	-	-	-	-	G	Q	F	C	H	K	P	C	C	H	K	P	C	P	P	P	G	E	R	K	A	R	D	C	T	V	FAS	
29	-	E	-	-	-	-	-	-	-	-	-	-	-	-	G	K	L	C	Q	M	C	C	Q	M	C	Q	Y	R	C	P	G	T	F	L	V	K	D	C	D	Q	CD27	
22	-	D	R	P	F	E	D	T	C	H	G	N	P	S	-	-	H	Y	D	K	A	V	R	L	C	C	Y	R	C	P	M	G	L	F	P	T	Q	Q	C	P	Q	CD30
24	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Q	Y	-	I	N	S	Q	C	C	S	L	N	C	Q	P	G	Q	K	L	V	S	D	C	-	CD40		
21	-	T	R	S	L	Q	D	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D	N	4-1BB		
33	-	G	-	-	-	-	-	-	-	-	-	-	-	-	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	R	OX40	
28	-	P	N	G	K	C	K	D	T	E	Y	K	R	H	N	-	-	-	-	-	-	-	L	C	C	L	S	C	P	P	G	T	Y	A	S	R	L	C	D	S	VC22	
26	-	S	N	G	K	C	K	D	N	E	Y	K	R	H	-	-	-	-	-	-	-	-	L	C	C	L	S	C	P	P	G	T	Y	A	S	R	L	C	D	S	CRMB	
27	-	V	R	G	V	A	E	T	P	T	Y	P	W	R	D	A	-	E	T	G	E	R	L	V	C	A	Q	C	P	P	G	T	F	V	Q	R	P	C	-	-	TNFR-6a	
27	-	V	R	G	V	A	E	T	P	T	Y	P	W	R	D	A	-	E	T	G	E	R	L	V	C	A	Q	C	P	P	G	T	F	V	Q	R	P	C	-	-	TNFR-6b	

FIG.3B

75	P	G	D	T	D	C	R	-	E	C	-	E	S	G	S	-	F	T	A	S	E	N	H	L	R	H	C	L	S	C	S	K	-	C	R	K	E	M	G	TNFR1		
68	T	K	T	S	D	T	V	C	-	D	S	C	-	E	D	S	T	Y	T	Q	L	W	N	W	V	P	E	C	L	S	C	G	S	-	C	S	D	Q	V	TNFR2		
60	N	Q	-	T	-	C	-	E	-	P	C	-	L	D	S	V	T	F	S	D	V	V	S	A	T	E	P	C	K	P	C	T	-	E	C	V	G	L	Q	S	NGFR	
73	S	R	S	Q	D	T	V	C	-	K	T	C	-	P	H	N	S	Y	N	E	H	W	N	H	L	S	T	C	Q	L	C	R	P	-	C	D	I	V	L	G	LTbR	
76	H	-	G	D	E	P	D	C	-	V	-	P	C	Q	E	G	K	E	Y	T	D	K	A	H	F	S	S	C	R	R	C	-	-	C	D	E	G	H	G	FAS		
56	H	R	K	A	-	A	Q	C	-	D	-	P	C	I	P	G	V	S	F	S	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD27		
61	R	-	-	P	T	D	C	-	R	K	C	-	-	E	P	D	Y	Y	L	D	E	A	D	R	C	T	A	C	V	T	C	S	-	-	-	R	D	D	-	CD30		
52	T	E	F	T	E	C	-	L	P	C	-	C	-	G	E	S	E	F	L	D	T	W	N	R	E	T	H	C	H	Q	K	Y	-	C	D	P	N	L	G	CD40		
40	N	R	N	Q	-	-	I	C	-	S	P	C	-	-	P	P	N	S	F	S	A	-	G	G	Q	R	-	P	C	I	C	R	-	Q	-	-	-	K	G	4-1BB		
59	S	Q	N	T	-	V	-	C	-	-	-	-	-	-	G	P	G	F	Y	N	D	V	V	S	S	K	-	P	C	K	T	-	W	C	-	N	L	R	S	OX40		
60	K	T	N	T	-	-	Q	C	-	T	P	C	-	-	G	S	G	T	F	T	G	R	N	N	H	L	P	A	C	L	S	C	N	G	R	C	N	Q	V	VC22		
58	K	T	N	T	N	T	Q	C	-	T	P	C	-	-	A	S	D	T	T	S	R	N	N	H	L	P	A	C	L	S	C	N	G	R	C	D	S	N	Q	V	CRMB	
63	R	R	D	S	P	T	T	C	-	G	P	C	-	-	P	P	R	H	Y	T	Q	F	W	N	Y	L	E	R	C	R	Y	C	N	V	L	C	G	E	R	E	E	TNFR-6a
63	R	R	D	S	P	T	T	C	-	G	P	C	-	-	P	P	R	H	Y	T	Q	F	W	N	Y	L	E	R	C	R	Y	C	N	V	L	C	G	E	R	E	E	TNFR-6b

FIG. 3C

111	-	Q	V	E	I	S	C	T	V	D	R	D	T	V	C	G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	Q	C	F	N	C	S	L	-	TNFR1		
106	-	-	-	E	T	Q	A	-	-	C	T	R	E	Q	N	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	-	-	G	C	R	L	C	A	P	L	TNFR2
95	M	S	A	P	-	-	-	C	V	E	A	D	D	A	V	C	R	C	A	Y	G	Y	-	Q	D	E	T	G	-	-	-	R	C	E	A	C	R	V	-	NGFR		
110	F	E	E	V	A	P	-	-	C	T	S	D	R	K	A	E	C	R	C	Q	P	G	M	S	C	V	Y	L	D	N	E	-	-	C	V	H	C	E	E	-	LTbR	
113	L	E	V	E	I	N	-	-	C	T	R	T	Q	N	T	K	C	R	C	K	P	N	-	-	-	-	-	-	-	-	-	-	-	-	F	F	C	N	-	-	FAS	
74	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D	H	T	R	P	-	-	H	C	E	S	C	R	H	-	-	CD27		
92	L	V	E	K	T	P	-	-	C	A	W	S	S	R	V	C	E	C	R	P	G	M	F	C	S	T	S	A	V	N	-	-	S	C	A	R	C	F	H	-	CD30	
89	L	R	V	Q	Q	K	-	-	G	T	S	E	T	D	T	I	C	T	C	E	G	W	H	C	T	-	-	S	E	A	-	-	-	C	E	S	C	V	L	H	-	CD40
71	V	F	R	T	R	K	E	-	C	S	S	T	S	H	A	E	C	D	C	T	P	G	F	H	C	L	-	-	G	A	-	-	G	C	S	M	C	E	Q	D	4-1BB	
92	G	S	E	R	K	Q	L	-	C	T	A	T	Q	D	T	V	C	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40	
96	-	-	E	T	R	S	-	-	C	N	T	T	H	H	R	I	C	E	C	S	P	G	Y	C	L	L	K	G	S	-	-	G	C	K	A	C	V	S	Q	-	VC22	
96	-	-	E	T	R	S	-	-	C	N	T	T	H	N	R	I	C	D	C	A	P	G	Y	C	F	L	K	G	S	-	-	G	C	K	A	C	V	S	Q	-	CRMB	
101	-	-	E	A	R	A	-	-	C	H	A	T	H	N	R	A	C	R	C	R	T	G	F	F	-	-	-	A	H	A	-	-	G	-	-	F	C	L	E	H	TNFR-6a	
101	-	-	E	A	R	A	-	-	C	H	A	T	H	N	R	A	C	R	C	R	T	G	F	F	-	-	-	A	H	A	-	-	G	-	-	F	C	L	E	H	TNFR-6b	

FIG.3D

**FIG. 3E**











264	T	K	P	L	A	P	N	P	S	F	S	P	T	P	G	F	T	P	T	L	G	F	S	P	V	P	S	S	T	F	T	S	S	T	Y	T	P	G	D	TNFR1	
294	-	-	-	-	-	-	-	L	Q	R	E	A	K	V	P	H	L	P	A	-	D	K	A	R	G	T	Q	G	P	E	Q	Q	H	L	L	I	T	A	-	TNFR2	
281	-	-	-	-	-	-	-	-	-	N	K	Q	G	A	N	S	R	P	P	-	N	Q	T	P	P	P	E	G	E	K	L	H	S	D	S	G	I	S	V	D	NGFR
262	-	-	-	-	-	-	-	-	P	E	G	E	S	P	P	C	P	A	-	P	R	A	D	P	H	F	F	D	L	A	E	P	L	-	-	-	-	-	-	LTbR	
212	-	-	-	-	-	S	P	T	L	N	P	E	-	-	-	-	T	V	A	I	N	L	S	D	V	D	L	S	K	Y	I	T	-	-	-	-	-	-	-	FAS	
169	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	P	CD27		
322	T	T	F	E	A	P	P	L	G	T	Q	P	D	C	N	P	T	P	E	-	N	G	E	A	P	A	S	T	S	P	T	Q	S	L	L	V	D	S	Q	A	CD30
222	-	-	-	-	-	-	-	-	P	T	N	K	A	P	H	P	K	Q	E	-	P	Q	-	E	I	N	F	P	D	-	-	-	-	-	-	-	-	-	-	CD40	
193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB		
198	-	-	-	-	-	-	-	-	-	T	S	Q	G	P	S	T	R	P	V	-	E	-	-	-	V	P	G	G	R	A	V	A	I	L	G	L	G	L	-	OX40	
255	-	-	-	-	-	-	-	-	L	N	F	E	I	K	C	N	N	-	-	-	-	-	-	K	G	S	-	-	S	F	K	Q	-	-	-	L	T	K	-	VC22	
255	-	-	-	-	-	-	-	-	L	N	F	E	I	K	C	N	N	-	-	-	-	-	-	K	D	S	Y	S	S	K	Q	-	-	-	L	T	K	-	CRMB		
229	-	-	-	-	-	-	-	-	L	Q	R	L	L	Q	A	L	E	A	P	E	-	G	W	-	-	G	P	-	-	-	-	-	-	-	-	-	T	-	-	TNFR-6a	
143	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	-	S	W	A	R	G	G	-	-	-	-	-	-	-	-	-	-	A	-	-	TNFR-6b	

FIG.3J



[illegible]

FIG. 3L

365	N	V	P	P	L	R	W	K	E	F	V	R	R	L	G	L	S	D	H	E	I	D	R	L	E	L	Q	N	G	R	C	L	R	E	A	Q	Y	S	M	L	TNFR1
372	P	G	G	H	G	T	Q	V	N	V	T	C	I	V	N	V	C	S	S	D	H	-	S	S	Q	A	S	S	Q	A	S	S	T	M	G	D	T	-	-	TNFR2	
355	A	G	D	T	W	R	H	L	A	G	E	L	G	I	H	V	G	S	V	T	F	T	H	E	A	C	P	V	R	-	-	-	-	-	-	A	L	L	NGFR		
327	P	G	E	H	G	Q	V	A	H	G	A	N	G	I	H	V	G	S	V	T	V	T	G	N	I	Y	I	N	G	P	V	L	G	G	T	-	-	-	LTr		
246	-	-	-	-	-	-	-	-	K	G	F	V	R	K	N	G	V	E	A	K	I	D	E	I	K	N	D	N	V	Q	D	T	A	E	Q	K	V	Q	L	L	FAS
214	-	-	-	-	-	R	R	K	Y	R	S	N	K	G	E	S	P	V	E	P	A	E	P	C	R	Y	S	C	P	R	-	-	-	-	-	-	-	-	-	CD27	
441	R	R	S	S	T	Q	L	R	S	G	A	S	V	T	E	P	V	A	E	E	R	G	L	M	S	Q	P	L	M	E	T	C	H	S	V	G	A	Y	L	CD30	
256	-	-	-	-	-	-	-	-	-	H	G	C	Q	P	V	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD40		
222	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB		
245	-	-	-	-	-	-	-	R	L	P	P	D	-	A	H	K	P	P	G	G	S	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40	
308	A	Q	D	Y	E	T	D	T	I	S	Y	R	V	G	N	V	L	D	D	S	H	M	P	G	S	C	N	I	H	K	-	-	-	-	-	-	-	-	-	VC22	
311	T	Q	D	Y	E	T	D	T	I	S	Y	H	V	G	N	V	L	D	V	D	S	H	M	P	G	R	C	D	T	H	K	-	-	-	-	-	-	-	-	CRMB	
282	-	-	-	-	-	-	-	-	-	-	-	V	A	R	M	P	G	L	E	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6a	
155	-	-	-	-	-	-	-	-	-	-	-	-	G	R	R	C	G	R	G	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b	

FIG.3M



FIG. 3N



FIG. 3P

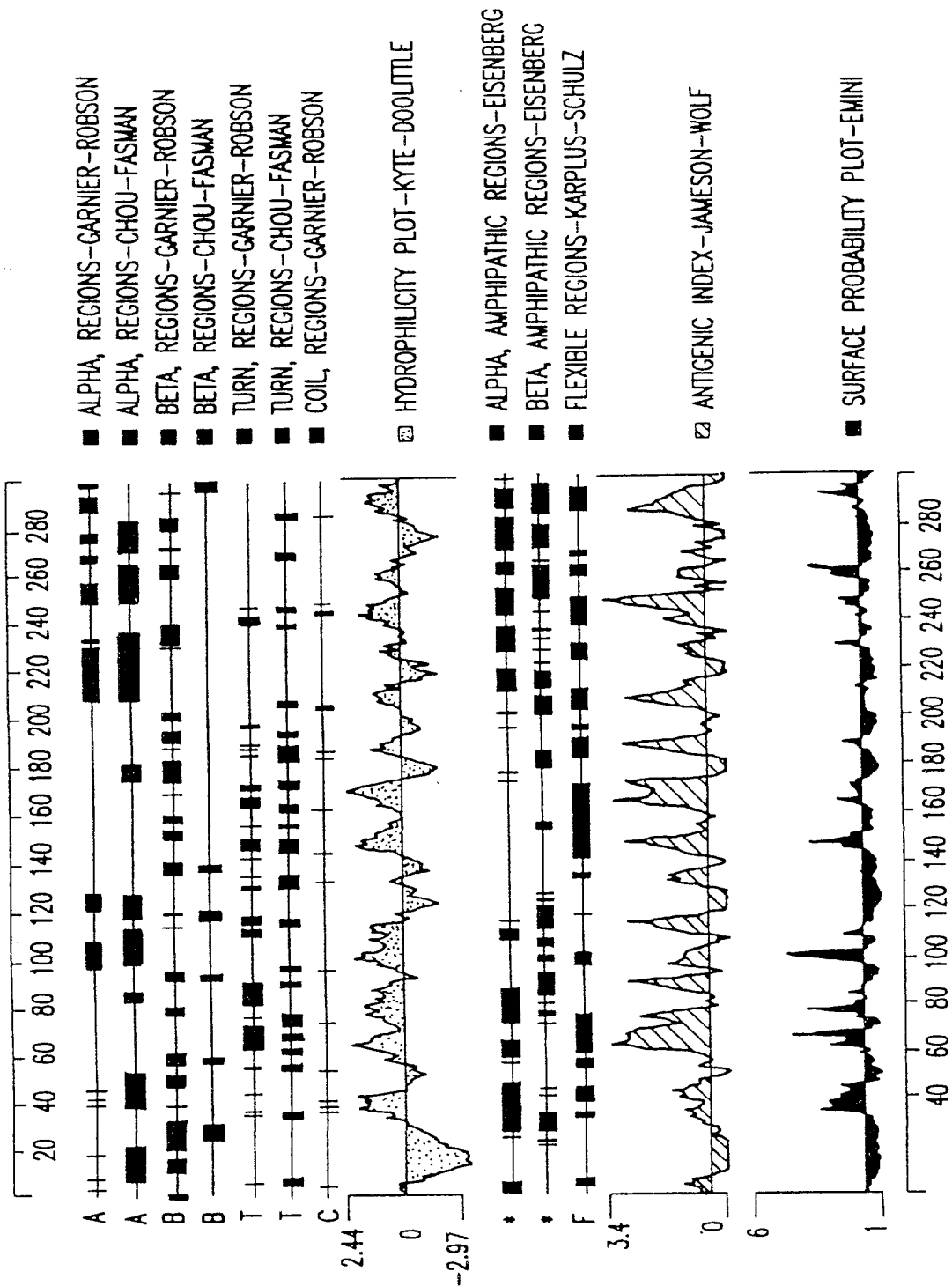


FIG.4

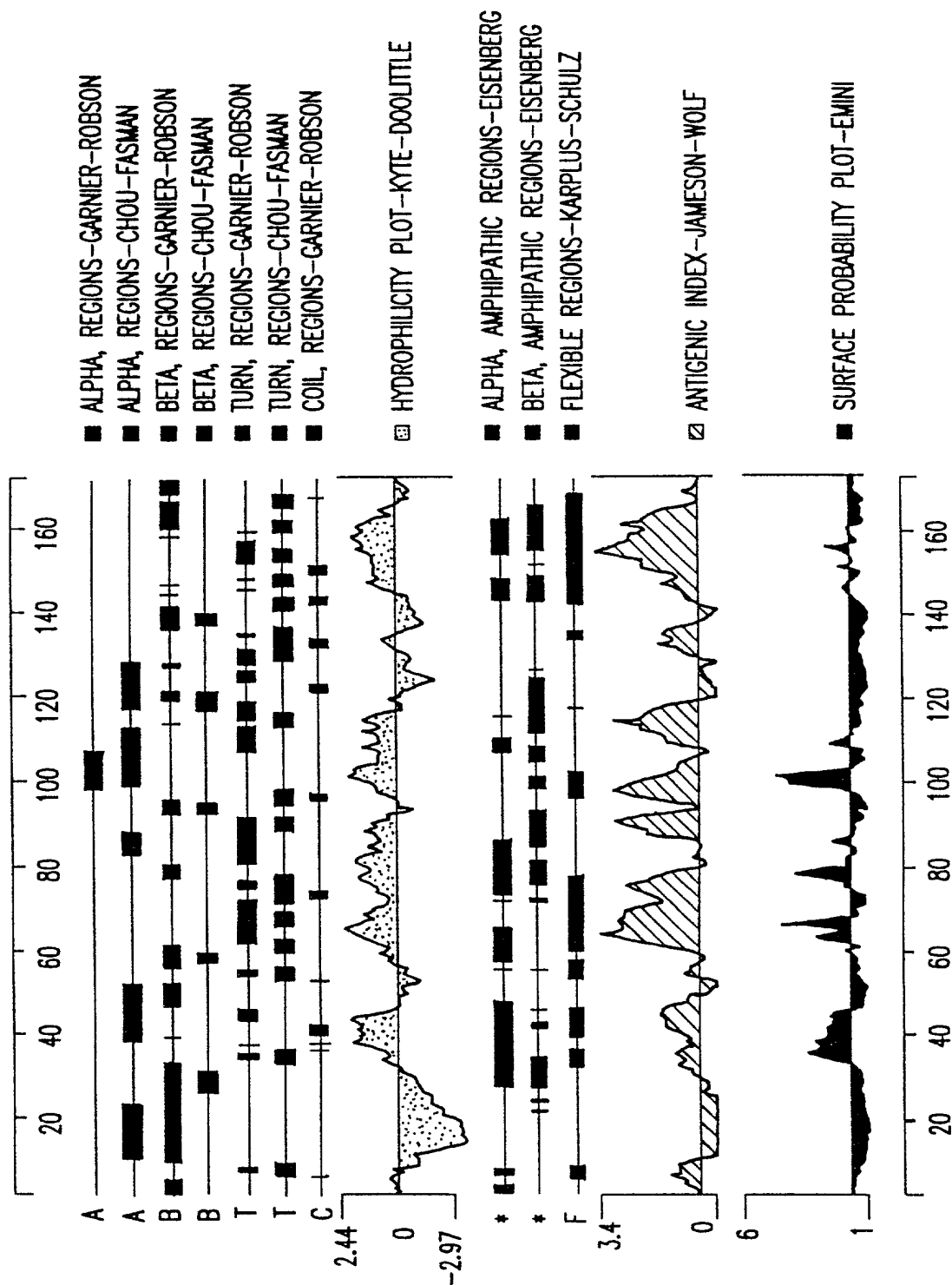


FIG.5

22/23

HELDI06R

GGCACGAGCA GGGTCCTGTN TCCGCCCTGA GCCGCGCTCT NCCTGCTCCA GCAAGGACCA  
TGAGGGCGCT GGAGGGGCCA GGCCTGTCGC TGCTGTGCCT GGTGTTGGCG CTGCCTGCCC  
TGCTGCCGGT GCCGGCTGTA CGCGGAGTGG CAGAAACACN NACNTACCCC TGGCGGGACG  
NAGAGACAGG GGAGCGGCTG GTGTNTNCCC ANTGCCCCC AGGCACCTTT NTGCAGCGGC  
CGTGCCGNCG AGACAGCCCC ACGACGTGTG GCCCGTNTCC ACCGCGCCAC TACACGCATT  
CTGGAACCTAC CTGGAGCGCT GNCGTTACTN CAACGTCCTC TCGGGGAGC GTNAGGAGGA  
GGCACGGGTT TNCCACGNCA ACCACAACCG NGGNTTACCG TNGCCGNACC GGTTCCTTCG  
NGGCAAGTTG GTTTTTNNTT TGGAGNAAGG ATTCGTGTTN CAATTNATTG ACGNAGTGAT  
TNNCNCGGG AAACNAAA

HCEOW38R

CGCAACTGCA CGGCCCTGGG ACTGGCCCTC AATGTGCCAG GNTCTTCCTC CCATGACACC  
CTGTGCACCA GCTGCACTGG CTTCCCCCTC AGCACCAGGG TACCANGAGC TGAGGAGTGT  
GAGCNTGCCG TCATCGACTT TTTGGCTTTC CAGGACATCT CCATCAAGAG GCTGCAGCGG  
CTGCTCANGC C

FIG.6

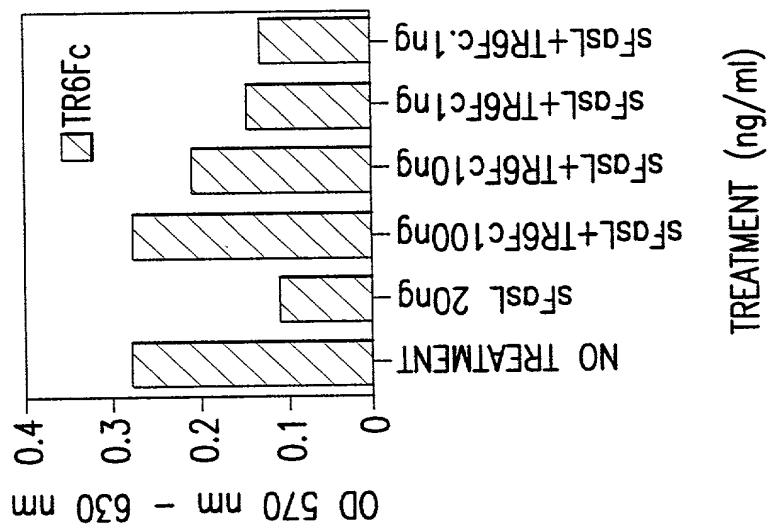


FIG. 7B

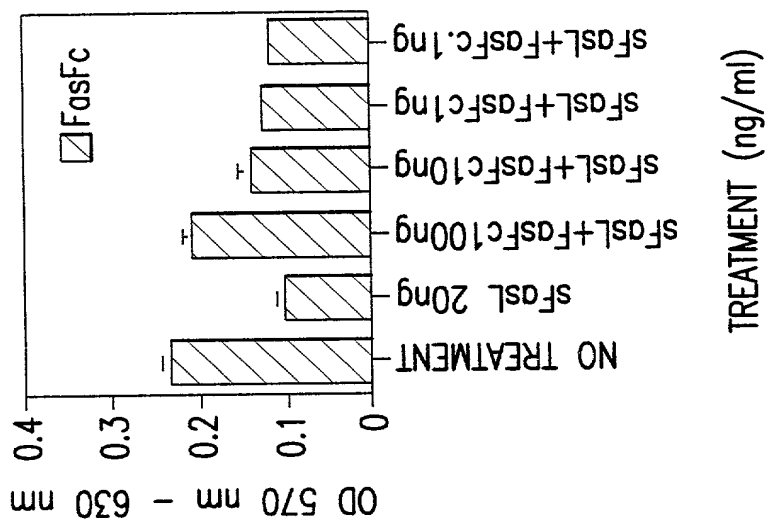


FIG. 7A